

SEULBERGER et al., Serial No. 09/462,629

specification and substitute replacement pages 28-32 attached hereto as separate pages.

REMARKS

A copy of the corrected Sequence Listing in computer readable form is attached hereto. The content of the paper copy of the Sequence Listing and the copy of the Sequence Listing in computer readable form is the same, and includes no new matter.

It is believed that by submitting the present amendment and sequence listing diskette, the application now fully complies with the requirements of 37 CFR 1.821-1.825. Favorable action by the examiner is solicited.

Please charge any shortage in fees due in connection with the filing of this paper, including Extension of Time fees to Deposit Account No. 11.0345. Please credit any excess fees to such deposit account.

Respectfully submitted,

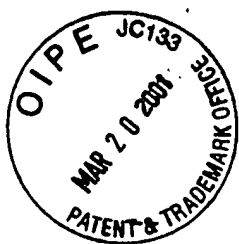
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SEQUENCE LISTING

<110> Seulberger, Harald
Lerchl, Jenms
Schmidt, Ralf-Michael
Krupinska, Karin
Falk, Jon

<120> DNA sequence encoding a hydroxyphenylpyruvate dioxygenase, and its
overproduction in plants

<140> US 09/462,629

<141> 2000-01-11

<150> PCT/EP98/03832

<151> 1998-06-23

<160> 2

<170> WordPerfect version 6.1

<210> 1

<211> 1565

<212> DNA

<213> hppd from barley

<220>

<221> CDS

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Ala Ala Val Thr Pro Glu His Ala Arg Pro His Arg Met Val Arg Phe	
15 20 25 30	
aac ccg cgc agc gac cgc ttc cac acg ctc tcc ttc cac cac gtc gag	146
Asn Pro Arg Ser Asp Arg Phe His Thr Leu Ser Phe His His Val Glu	
35 40 45	
ttc tgg tgc gcg gac gcc gcc tcc gcc gcc ggc cgc ttc gcg ttc gcg	194
Phe Trp Cys Ala Asp Ala Ala Ser Ala Ala Gly Arg Phe Ala Phe Ala	
50 55 60	
ctc ggc gcg ccg ctc gcc gcc agg tcc gac ctc tcc acg ggg aac tcc	242
Leu Gly Ala Pro Leu Ala Ala Arg Ser Asp Leu Ser Thr Gly Asn Ser	
65 70 75	
gcg cac gcc tcc cag ctg ctc cgc tcg ggc tcc ctc gcc ttc ctc ttc	290

Ala	His	Ala	Ser	Gln	Leu	Leu	Arg	Ser	Gly	Ser	Leu	Ala	Phe	Leu	Phe	
80						85					90					
acc	gcg	ccc	tac	gcc	aac	ggc	tgc	gac	gcc	gcc	acc	gcc	tcc	ctg	ccc	338
Thr	Ala	Pro	Tyr	Ala	Asn	Gly	Cys	Asp	Ala	Ala	Thr	Ala	Ser	Leu	Pro	
95					100				105						110	
tcc	ttc	tcc	gcc	gac	gcc	gcg	cgc	cgg	ttc	tcc	gcc	gac	cac	ggg	atc	386
Ser	Phe	Ser	Ala	Asp	Ala	Ala	Arg	Arg	Phe	Ser	Ala	Asp	His	Gly	Ile	
				115					120					125		
gcg	gtg	cgc	tcc	gta	gcg	ctg	cgc	gtc	gca	gac	gcc	gcc	gag	gcc	ttc	434
Ala	Val	Arg	Ser	Val	Ala	Leu	Arg	Val	Ala	Asp	Ala	Ala	Glu	Ala	Phe	
			130					135					140			
cgc	gcc	agt	cgt	cga	cgg	ggc	gcg	cgc	ccg	gcc	ttc	gcc	ccc	gtg	gac	482
Arg	Ala	Ser	Arg	Arg	Arg	Gly	Ala	Arg	Pro	Ala	Phe	Ala	Pro	Val	Asp	
		145				150					155					
ctc	ggc	cgc	ggc	ttc	gcg	ttc	gcg	gag	gtc	gag	ctc	tac	ggc	gac	gtc	530
Leu	Gly	Arg	Gly	Phe	Ala	Phe	Ala	Glu	Val	Glu	Leu	Tyr	Gly	Asp	Val	
160						165					170					
gtg	ctc	cgc	ttc	gtc	agc	cac	ccg	gac	ggc	acg	gac	gtg	ccc	ttc	ttg	578
Val	Leu	Arg	Phe	Val	Ser	His	Pro	Asp	Gly	Thr	Asp	Val	Pro	Phe	Leu	
175					180				185						190	
ccg	ggg	ttc	gag	ggc	gta	acc	aac	ccg	gac	gcc	gtg	gac	tac	ggc	ctg	626
Pro	Gly	Phe	Glu	Gly	Val	Thr	Asn	Pro	Asp	Ala	Val	Asp	Tyr	Gly	Leu	
				195				200						205		
acg	cgg	ttc	gac	cac	gtc	gtc	ggc	aac	gtc	ccg	gag	ctt	gcc	ccc	gcc	674
Thr	Arg	Phe	Asp	His	Val	Val	Gly	Asn	Val	Pro	Glu	Leu	Ala	Pro	Ala	
			210				215						220			
gca	gcc	tac	atc	gcc	ggg	ttc	acg	ggg	ttc	cac	gag	ttc	gcc	gag	ttc	722
Ala	Ala	Tyr	Ile	Ala	Gly	Phe	Thr	Gly	Phe	His	Glu	Phe	Ala	Glu	Phe	
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Thr	Ala	Glu	Asp	Val	Gly	Thr	Thr	Glu	Ser	Gly	Leu	Asn	Ser	Val	Val	
		240				245					250					
ctc	gcc	aac	aac	tcg	gag	ggc	gtg	ctg	ctg	ccg	ctc	aac	gag	ccg	gtg	818
Leu	Ala	Asn	Asn	Ser	Glu	Gly	Val	Leu	Leu	Pro	Leu	Asn	Glu	Pro	Val	
255					260					265					270	
cac	ggc	acc	aag	cgc	cgg	agc	cag	ata	cag	acg	ttc	ctg	gaa	cac	cac	866
His	Gly	Thr	Lys	Arg	Arg	Ser	Gln	Ile	Gln	Thr	Phe	Leu	Glu	His	His	
				275					280					285		
ggc	ggc	ccg	ggc	gtg	cag	cac	atc	gcg	gtg	gcc	agc	agt	gac	gtg	ctc	914
Gly	Gly	Pro	Gly	Val	Gln	His	Ile	Ala	Val	Ala	Ser	Ser	Asp	Val	Leu	

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agg acg ctc agg aag atg cgt gcg cgc tcc gcc atg ggc ggc ttc gac			962
Arg Thr Leu Arg Lys Met Arg Ala Arg Ser Ala Met Gly Gly Phe Asp			
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ttc ctg cca ccc ccg ctg ccg aag tac tac gaa ggc gtg cga cgc ctt			1010
Phe Leu Pro Pro Pro Leu Pro Lys Tyr Tyr Glu Gly Val Arg Arg Leu			
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gcc ggg gat gtc ctc tcg gag gcg cag atc aag gaa tgc cag gag ctg			1058
Ala Gly Asp Val Leu Ser Glu Ala Gln Ile Lys Glu Cys Gln Glu Leu			
335	340	345	350
ggg gtg ctc gtc gat agg gac gac caa ggg gtg ttg ctc caa atc ttc			1106
Gly Val Leu Val Asp Arg Asp Asp Gln Gly Val Leu Leu Gln Ile Phe			
355	360	365	
acc aag cca gta ggg gac agg ccg acc ttg ttc ctg gag atg atc cag			1154
Thr Lys Pro Val Gly Asp Arg Pro Thr Leu Phe Leu Glu Met Ile Gln			
370	375	380	
agg atc ggg tgc atg gag aag gac gag aga ggg gaa gag tac cag aag			1202
Arg Ile Gly Cys Met Glu Lys Asp Glu Arg Gly Glu Glu Tyr Gln Lys			
385	390	395	
ggg ggc tgc ggc ggg ttc ggc aaa ggc aac ttc tcc gag ctg ttc aag			1250
Gly Gly Cys Gly Gly Phe Gly Lys Gly Asn Phe Ser Glu Leu Phe Lys			
400	405	410	
tcc att gaa gat tac gag aag tcc ctt gaa gcc aag caa tct gct gca			1298
Ser Ile Glu Asp Tyr Glu Lys Ser Leu Glu Ala Lys Gln Ser Ala Ala			
415	420	425	430
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gaagctgaag acagatgtat cctatgtatg atgggtgtaa tggatggtag aggggctcac			1470
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<213> hppd from barley

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 35 40 45
 Cys Ala Asp Ala Ala Ser Ala Ala Gly Arg Phe Ala Phe Ala Leu Gly
 50 55 60
 Ala Pro Leu Ala Ala Arg Ser Asp Leu Ser Thr Gly Asn Ser Ala His
 65 70 75 80
 Ala Ser Gln Leu Leu Arg Ser Gly Ser Leu Ala Phe Leu Phe Thr Ala
 85 90 95
 Pro Tyr Ala Asn Gly Cys Asp Ala Ala Thr Ala Ser Leu Pro Ser Phe
 100 105 110
 Ser Ala Asp Ala Ala Arg Arg Phe Ser Ala Asp His Gly Ile Ala Val
 115 120 125
 Arg Ser Val Ala Leu Arg Val Ala Asp Ala Ala Glu Ala Phe Arg Ala
 130 135 140
 Ser Arg Arg Arg Gly Ala Arg Pro Ala Phe Ala Pro Val Asp Leu Gly
 145 150 155 160
 Arg Gly Phe Ala Phe Ala Glu Val Glu Leu Tyr Gly Asp Val Val Leu
 165 170 175
 Arg Phe Val Ser His Pro Asp Gly Thr Asp Val Pro Phe Leu Pro Gly
 180 185 190
 Phe Glu Gly Val Thr Asn Pro Asp Ala Val Asp Tyr Gly Leu Thr Arg
 195 200 205
 Phe Asp His Val Val Gly Asn Val Pro Glu Leu Ala Pro Ala Ala Ala
 210 215 220
 Tyr Ile Ala Gly Phe Thr Gly Phe His Glu Phe Ala Glu Phe Thr Ala
 225 230 235 240
 Glu Asp Val Gly Thr Thr Glu Ser Gly Leu Asn Ser Val Val Leu Ala
 245 250 255
 Asn Asn Ser Glu Gly Val Leu Leu Pro Leu Asn Glu Pro Val His Gly
 260 265 270
 Thr Lys Arg Arg Ser Gln Ile Gln Thr Phe Leu Glu His His Gly Gly
 275 280 285

Pro Gly Val Gln His Ile Ala Val Ala Ser Ser Asp Val Leu Arg Thr
 290 295 300

Leu Arg Lys Met Arg Ala Arg Ser Ala Met Gly Gly Phe Asp Phe Leu
 305 310 315 320

Pro Pro Pro Leu Pro Lys Tyr Tyr Glu Gly Val Arg Arg Leu Ala Gly
 325 330 335

Asp Val Leu Ser Glu Ala Gln Ile Lys Glu Cys Gln Glu Leu Gly Val
 340 345 350

Leu Val Asp Arg Asp Asp Gln Gly Val Leu Leu Gln Ile Phe Thr Lys
 355 360 365

Pro Val Gly Asp Arg Pro Thr Leu Phe Leu Glu Met Ile Gln Arg Ile
 370 375 380

Gly Cys Met Glu Lys Asp Glu Arg Gly Glu Glu Tyr Gln Lys Gly Gly
 385 390 395 400

Cys Gly Gly Phe Gly Lys Gly Asn Phe Ser Glu Leu Phe Lys Ser Ile
 405 410 415

Glu Asp Tyr Glu Lys Ser Leu Glu Ala Lys Gln Ser Ala Ala Val Gln
 420 425 430

Gly Ser--.